

Serial Number: 10/070,412CRF Processing Date: 2/8/2002
Edited by: PCF/10
Verified by: PCF/10 (STIC staff)**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☒ Inserted mandatory headings, specifically: C2207 Seq. 2
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



PCT10

RAW SEQUENCE LISTING

DATE: 07/18/2002

PATENT APPLICATION: US/10/070,412

TIME: 21:58:57

Input Set : N:\Crf3\07152002\J070412.raw

Output Set: N:\CRF3\07182002\J070412.raw

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1 <110> APPLICANT: AstaCarotene AB
2 <120> TITLE OF INVENTION: DNA construct and its use
3 <130> FILE REFERENCE: 29295-AstaCarotene
4 <140> CURRENT APPLICATION NUMBER: US/10/070,412
5 <141> CURRENT FILING DATE: 2002-06-12
6 <160> NUMBER OF SEQ ID NOS: 2
7 <170> SOFTWARE: PatentIn Ver. 2.1
9 <210> SEQ ID NO: 1
10 <211> LENGTH: 2543
11 <212> TYPE: DNA
12 <213> ORGANISM: Artificial Sequence
13 <220> FEATURE:
14 <223> OTHER INFORMATION: Description of Artificial Sequence: napin promoter
15 + chloroplast localization signal + beta-carotene C-4 oxygenase
16 coding sequence + termination sequence
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18 <221> NAME/KEY: promoter
19 <222> LOCATION: (1)..(1145)
20 <220> FEATURE:
21 <221> NAME/KEY: transit_peptide
22 <222> LOCATION: (1179)..(1347)
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1179)..(2217)
26 <220> FEATURE:
27 <221> NAME/KEY: terminator
28 <222> LOCATION: (2273)..(2536)
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32 ttcccaaat tttaaatttc actattggctt gaatgctttct tctttgagga agaaacaatt 180
33 cagatggcag aaatgtatca accaatgcat atatacaaat gtacctcttg ttctcaaaac 240
34 atctatcgga tggttccatt tgttttgta tcoaattagt gactacttta tattattcac 300
35 tctcttttat tactattttc atgcgaggtt gccatgtaca ttatatattgt aaggattgac 360
36 gctattgagc gtttttcttc aattttcttt attttagaca tggggtatgaa atgtgtgtta 420
37 gagtggggtt gaatgagata tacgttcaag tgaagtggca tacggttctc gagtaaggat 480
38 gacctaccoc ttcttgagac aaatgttaca ttttagtata agagtaaaat gtgtacctat 540
39 aactcaaaat cgaattgacat gtatccattc aacataaaat taaaccagcc tgcacctgca 600
40 tccacatttc aagtatatttc aaaccgttcg gctctatcc accgggtgta acaagacgga 660
41 ttccgaattt ggaagatttt gactcaaaat cccaatttat attgaccgtg actaaatcaa 720
42 ctttaacttc tataattctg attaagctcc caatttata tcccaacggc actacctcca 780
43 aaatttatag actctcatcc ccttttaaac caacttagta aacgtttttt tttttaattt 840
44 tatgaagtta agttttttac ttgtttttaa aaagaatcgt tcataagatg ccatgccaga 900

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45  acattagcta cactgtacac atagcatgca gccgcggaga attgtttttc ttgcccaact 960
46  gtcactccct tcaaacacct aagagcttct ctctcacagc acacacatac aatcacatgc 1020
47  gtgcattgat tattacacgt gatgccatg caaatctcct ttatagccta taaattaaact 1080
48  catccgcttc actctttact caaaccaaaa ctcatcaata caaacagaat taaaaacata 1140
49  caccgaggatc ctacgtcaca caaagagtaa agaagaaca atg gct tcc tct atg 1194
50                                     Met Ala Ser Ser Met
51                                     1           5
52  ctc tct tcc gct act atg gtt gcc tct ccg gct cag gcc act atg gtc 1242
53  Leu Ser Ser Ala Thr Met Val Ala Ser Pro Ala Gln Ala Thr Met Val
54                                     10          15          20
55  gct cct ttc aac gga ctt aag tcc tcc gct gcc ttc cca gcc acc cgc 1290
56  Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala Phe Pro Ala Thr Arg
57                                     25          30          35
58  aag gct aac aac gac att act tcc atc aca agc aac gcc gga cgc gtt 1338
59  Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser Asn Gly Gly Arg Val
60                                     40          45          50
61  aac tgc atg tct aga atg cca tcc gag tgc tca gac gca gct cgt cct 1386
62  Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro
63                                     55          60          65
64  gcg cta aag cac gcc tac aaa cct cca gca tct gac gcc aag gcc atc 1434
65  Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile
66                                     70          75          80          85
67  acg atg gcg ctg acc atc att gcc acc tgg acc gca gtg ttt tta cac 1482
68  Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His
69                                     90          95          100
70  gca ata ttt caa atc agg cta ccg aca tcc atg gac cag ctt cac tgg 1530
71  Ala Ile Phe Gln Ile Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp
72                                     105         110         115
73  ttg cct gtg tcc gaa gcc aca gcc cag ctt ttg gcc gga agc agc agc 1578
74  Leu Pro Val Ser Glu Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser
75                                     120         125         130
76  cta ctg cac atc get gca gtc ttc att gta ctt gag ttc ctg tac act 1626
77  Leu Leu His Ile Ala Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr
78                                     135         140         145
79  ggt cta ttc atc acc aca cat gac gca atg cat gcc acc ata gct ttg 1674
80  Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Leu
81                                     150         155         160         165
82  agg cac agg cag ctg aat gat ctg ctt gcc aac atc tgc ata tca ctg 1722
83  Arg His Arg Gln Leu Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu
84                                     170         175         180
85  tac gcc tgg ttt gac tac agc atg ctg cat cgc aag cac tgg gag cac 1770
86  Tyr Ala Trp Phe Asp Tyr Ser Met Leu His Arg Lys His Trp Glu His
87                                     185         190         195
88  cac aac cat act gcc gaa gtg ggg aaa gac cct gac ttc cac aag gga 1818
89  His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly
90                                     200         205
91  aat ccc gcc ctt gtc ccc tgg ttc gcc agc ttc atg tcc agc tac atg 1866
92  Asn Pro Gly Leu Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met
93                                     215         220         225

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94   tcc ctg tgg cag ttt gcc cgg ctg gca tgg tgg gca gtg atg caa   1914
95   Ser Leu Trp Gln Phe Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln
96   230                               235           240           245
97   atg ctg ggg gcg ccc atg gca aat ctc cta gtc ttc atg gct gca gcc   1962
98   Met Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala
99   250                               255           260
100  cca atc ttg tca gca ttc cgc ctc ttc tac ttc ggc act tac ctg cca   2010
101  Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro
102  265                               270           275
103  cac aag cct gag cca ggc cct gca gca ggc tct cag gtg atg gcc tgg   2058
104  His Lys Pro Glu Pro Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp
105  280                               285           290
106  ttc agg gcc aag aca agt gag gca gca ggc tct gat gtg atg agt ttc ctg aca   2106
107  Phe Arg Ala Lys Thr Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr
108  295                               300           305
109  tgc tac cac ttt gac ctg cac tgg gag cac cac aga tgg ccc ttt gcc   2154
110  Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala
111  310                               315           320           325
112  ccc tgg tgg cag ctg ccc cac tgc cgc cgc ctg tcc ggg cgt ggc ctg   2202
113  Pro Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu
114  330                               335           340
115  gtg cct gcc ttg gca tgacctggtc cctccgctgg tgaccacagcg tctgcacaag   2257
116  Val Pro Ala Leu Ala
117  345
118  agtgcctagg agctcgaatt tccccgatcg ttcaaacatt tggcaataaa gtttcttaag 2317
119  attgaatcct gttgccggtc ttgcgatgat tatcatataa ttctgtttga attacgttaa 2377
120  gcatgtaata attaacatgt aatgcatgac gttatttatg agatgggttt ttatgattag 2437
121  agtcccgcaa ttatacattt aatacgcgat agaaaaacaaa atatagcgcg caaactagga 2497
122  taaattatcg cgcgcggtgt catctatggt actagatcgg gaattc           2543
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125  <211> LENGTH: 346
126  <212> TYPE: PRP
127  <213> ORGANISM: Artificial Sequence
128  <220> FEATURE:
129  <223> OTHER INFORMATION: Description of Artificial Sequence: deduced fusion
130  protein of transit peptide + peptide with beta-carotene C-4 oxygenase
131  activity
132  <400> SEQUENCE: 2
133  Met Ala Ser Ser Met Leu Ser Ser Ala Thr Met Val Ala Ser Pro Ala
134  1 5 10 15
135  Gln Ala Thr Met Val Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala
136  20 25 30
137  Phe Pro Ala Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser
138  35 40 45
139  Asn Gly Gly Arg Val Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser
140  50 55 60
141  Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser
142  65 70 75 80
143  Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr

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144		85		90		95	
145	Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro Thr Ser Met						
146		100		105		110	
147	Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala Gln Leu Leu						
148		115		120		125	
149	Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe Ile Val Leu						
150		130		135		140	
151	Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His						
152		145		150		155	
153	Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu Leu Gly Asn						
154		165		170		175	
155	Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met Leu His Arg						
156		180		185		190	
157	Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro						
158		195		200		205	
159	Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala Ser Phe						
160		210		215		220	
161	Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala Trp Trp						
162		225		230		235	
163	Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn Leu Leu Val						
164		245		250		255	
165	Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe						
166		260		265		270	
167	Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala Gly Ser						
168		275		280		285	
169	Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser Asp Val						
170		290		295		300	
171	Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His						
172		305		310		315	
173	Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys Arg Arg Leu						
174		325		330		335	
175	Ser Gly Arg Gly Leu Val Pro Ala Leu Ala						
176		340		345			

VERIFICATION SUMMARY

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